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1633

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/103,287A

DATE: 04/07/2000
TIME: 15:30:30

Input Set: **I103287A.RAW**

> This Raw Listing contains the General Information
> Section and up to first 5 pages.

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 1   <110> APPLICANT: Wallis, Nicola G.
 2         Burnham, Martin K. R.
 3   <120> TITLE OF INVENTION: MurC
 4   <130> FILE REFERENCE: GM10025
 5   <140> CURRENT APPLICATION NUMBER: US/09/103,287A
 6   <141> CURRENT FILING DATE: 1998-06-23
 7   <150> EARLIER APPLICATION NUMBER: US 60/052,720
 8   <151> EARLIER FILING DATE: 1997-07-03
 9   <160> NUMBER OF SEQ ID NOS: 6
10   <170> SOFTWARE: FastSEQ for Windows Version 4.0
11   <210> SEQ ID NO 1
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13   <212> TYPE: DNA
14   <213> ORGANISM: Staphylococcus aureus
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17         atgagttcat tagcacaaat catgcatgat ttaggacatg aagttcaagg atcggatatt     120
18         gagaactacg tatttacaga agttgctctt agaaataagg ggataaaaat attaccattt     180
19         ggtgctaata acataaaaga agatatggta gttatacaag gtaatgcatt cgcgagtagc     240
20         catgaagaaa tagtacgtgc acatcaattg aaattagatg ttgtaagtta taatgatttt     300
21         ttaggacaga ttattgatca atatacttca gtagctgtaa ctggtgcaca tggtaaaact     360
22         tctacaacag gtttattatc acatgttatg aatggtgata aaaagacttc atttttaatt     420
23         ggtgatggca caggtatggg attgcctgaa agtgattatt cgcttttga ggcatgtgaa     480
24         tatagacgtc acttttaag ttataaacct gattacgcaa ttatgacaaa tattgatttc     540
25         gatcatcctg attatttcaa agatattaat gatgtttttg atgcattcca agaaatggca     600
26         cataatgtta aaaaggtat tattgcttgg ggtgatgatg aacatctacg taaaattgaa     660
27         gcagatgttc caatttatta ctatggattt aaagattcgg atgacattta tgctcaaaat     720
28         attcaaatta cggataaagg tactgctttt gatgtgtatg tggatggtga gtttttatgat     780
29         cacttcctgt ctccacaata tggtgaccat acagttttaa atgcattagc tgtaattgcg     840
30         attagttatt tagagaagct agatgttaca aatattaaag aagcattaga aacgtttggt     900
31         ggtgttaaac gtcgtttcaa tgaaactaca attgcaaatc aagttattgt agatgattat     960
32         gcacaccatc caagagaaat tagtgctaca attgacacag cacgaaagaa atatccacat    1020
33         aaagaagttg ttgcagtatt tcaaccacac actttctcta gaacacaagc atttttaaat    1080
34         gaatttgcag aaagtttatg taaagcagat cgtgtattct tatgtgaaat ttttggctca    1140
35         attagagaaa attctggcgc attaacgata caagatttaa ttgataaaat tggaggtgca    1200
36         tcgttcatta atgaagatct tattaatgta ttagaacaat ttgataatgc tgttgtttta    1260
37         tttatgggtg caggtgatat tcaaaaatta caaaatgcat atttagataa attaggcatg    1320
38         aaaaatgcgt tttaatatgt ttataataga g                                 1351
39   <210> SEQ ID NO 2
40   <211> LENGTH: 437
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42   <213> ORGANISM: Staphylococcus aureus
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47                20                  25                  30
48        Ile Glu Asn Tyr Val Phe Thr Glu Val Ala Leu Arg Asn Lys Gly Ile
49                35                  40                  45
50        Lys Ile Leu Pro Phe Gly Ala Asn Asn Ile Lys Glu Asp Met Val Val
51                50                  55                  60
52        Ile Gln Gly Asn Ala Phe Ala Ser Ser His Glu Glu Ile Val Arg Ala
53        65                  70                  75                  80
54        His Gln Leu Lys Leu Asp Val Val Ser Tyr Asn Asp Phe Leu Gly Gln
55                    85                  90                  95
56        Ile Ile Asp Gln Tyr Thr Ser Val Ala Val Thr Gly Ala His Gly Lys
57                100                 105                 110
58        Thr Ser Thr Thr Gly Leu Leu Ser His Val Met Asn Gly Asp Lys Lys
59                115                 120                 125
60        Thr Ser Phe Leu Ile Gly Asp Gly Thr Gly Met Gly Leu Pro Glu Ser
61                130                 135                 140
62        Asp Tyr Phe Ala Phe Glu Ala Cys Glu Tyr Arg Arg His Phe Leu Ser
63        145                 150                 155                 160
64        Tyr Lys Pro Asp Tyr Ala Ile Met Thr Asn Ile Asp Phe Asp His Pro
65                165                 170                 175
66        Asp Tyr Phe Lys Asp Ile Asn Asp Val Phe Asp Ala Phe Gln Glu Met
67                180                 185                 190
68        Ala His Asn Val Lys Lys Gly Ile Ile Ala Trp Gly Asp Asp Glu His
69                195                 200                 205
70        Leu Arg Lys Ile Glu Ala Asp Val Pro Ile Tyr Tyr Tyr Gly Phe Lys
71                210                 215                 220
72        Asp Ser Asp Asp Ile Tyr Ala Gln Asn Ile Gln Ile Thr Asp Lys Gly
73        225                 230                 235                 240
74        Thr Ala Phe Asp Val Tyr Val Asp Gly Glu Phe Tyr Asp His Phe Leu
75                245                 250                 255
76        Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala Val Ile
77                260                 265                 270
78        Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys Glu Ala
79                275                 280                 285
80        Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr Thr Ile
81                290                 295                 300
82        Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg Glu Ile
83        305                 310                 315                 320
84        Ser Ala Thr Ile Asp Thr Ala Arg Lys Lys Tyr Pro His Lys Glu Val
85                325                 330                 335
86        Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala Phe Leu
87                340                 345                 350
88        Asn Glu Phe Ala Glu Ser Leu Cys Lys Ala Asp Arg Val Phe Leu Cys
89                355                 360                 365
90        Glu Ile Phe Gly Ser Ile Arg Glu Asn Ser Gly Ala Leu Thr Ile Gln
91                370                 375                 380
92        Asp Leu Ile Asp Lys Ile Gly Gly Ala Ser Phe Ile Asn Glu Asp Leu
93        385                 390                 395                 400
94        Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Val Leu Phe Met Gly
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 95                         405                410                415
 96        Ala Gly Asp Ile Gln Lys Leu Gln Asn Ala Tyr Leu Asp Lys Leu Gly
 97                         420                425                430
 98        Met Lys Asn Ala Phe
 99                   435
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101   <211> LENGTH: 660
102   <212> TYPE: DNA
103   <213> ORGANISM: Staphylococcus aureus
104   <400> SEQUENCE: 3
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106        tgttgatgtg tatgtggatg gtgagtttta tgatcacttc ctgtctccac aatatggtga     120
107        ccatacagtt ttaaatgcat tagctgtaat tgcgattagt tatttagaga agctagatgt     180
108        tacaaatatt aaagaagcat tagaaacgtt tggtggtgtt aaacgtcgtt tcaatgaaac     240
109        tacaattgca aatcaagtta ttgtagatga ttatgcacac catccaagag aaattagtgc     300
110        tacaattgac acagcacgaa agaaatatcc acataaagaa gttgttgcag tatttcaacc     360
111        acacactttc tctagaacac aagcattttt aaatgaattt gcagaaagtt taagtaaagc     420
112        agatcgtgta ttcttatgtg aaattttttgg atcaattaga gaaaatactg gcgcattaac     480
113        gatacaagat ttaattgata aaattgaagg tgcatcgtta attaatgaag attctattaa     540
114        tgtattagaa caatttgata atgctgttgt tttatttatg ggtgcaggtg atattcaaaa     600
115        attacaaaat gcatatttag ataaattagg catgaaaaat gcgtttttaat atgtttataa     660
116   <210> SEQ ID NO 4
117   <211> LENGTH: 215
118   <212> TYPE: PRT
119   <213> ORGANISM: Staphylococcus aureus
120   <400> SEQUENCE: 4
121        Phe Lys Asp Ser Asp Asp Ile Tyr Ala Gln Ile Phe Gln Ile Thr Asp
122        1               5                   10                  15
123        Lys Gly Thr Ala Val Asp Val Tyr Val Asp Gly Glu Phe Tyr Asp His
124                        20                  25                  30
125        Phe Leu Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala
126                        35                  40                  45
127        Val Ile Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys
128          50                  55                  60
129        Glu Ala Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr
130        65                  70                  75                  80
131        Thr Ile Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg
132                        85                  90                  95
133        Glu Ile Ser Ala Thr Ile Asp Thr Ala Arg Lys Lys Tyr Pro His Lys
134                        100                 105                 110
135        Glu Val Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala
136                        115                 120                 125
137        Phe Leu Asn Glu Phe Ala Glu Ser Leu Ser Lys Ala Asp Arg Val Phe
138                        130                 135                 140
139        Leu Cys Glu Ile Phe Gly Ser Ile Arg Glu Asn Thr Gly Ala Leu Thr
140        145                 150                 155                 160
141        Ile Gln Asp Leu Ile Asp Lys Ile Glu Gly Ala Ser Leu Ile Asn Glu
142                        165                 170                 175
143        Asp Ser Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Val Leu Phe
144                        180                 185                 190
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148                   210                 215
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150    <211> LENGTH: 19
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152    <213> ORGANISM: Staphylococcus aureus
153    <400> SEQUENCE: 5
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156    <211> LENGTH: 19
157    <212> TYPE: DNA
158    <213> ORGANISM: Staphylococcus aureus
159    <400> SEQUENCE: 6
160          gttacaaata ttaaagaag                                              19
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VERIFICATION SUMMARY
ENT APPLICATION **US/09/103 87A**

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TIME: 15:30:30

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